

FIGURE 3A

original1	BCY1	1	-----GCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	110
MC50A19	BCY I	(1)	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	
MC50A6	BCY I	(1)	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	
MC50A8	BCY I	(1)	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	
MC54.21	BCY I	(1)	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	
MC55.29	BCY I	(1)	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	
MC55.32	BCY I	(1)	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	
Consensus		111	ATGSCCGAGTGGCGCTGAAGGGCAGCAGCAACACACGGAGTGTGTTCCCTGTCCACCTCCGACACAGCTGGCTGAGATCTGTGGGCAAGGCAGAGCTGCAAGATTAGGC	220
original1	BCY1	(108)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
MC50A19	BCY I	(111)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
MC50A6	BCY I	(111)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
MC50A8	BCY I	(111)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
MC54.21	BCY I	(111)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
MC55.29	BCY I	(111)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
MC55.32	BCY I	(111)	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	
Consensus		221	CTTGAAGGCCAAGAACCAACACCTACATCATAGACACACCGGTGAGGGGCGAGGAACCAACCTGTTTCATGTTGTCACAGGGCAACGGAGGACACTGGCCACAGCCCCGGGCGGGAATATCA	330
original1	BCY1	(218)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
MC50A19	BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
MC50A6	BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
MC50A8	BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
MC54.21	BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
MC55.29	BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
MC55.32	BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	
Consensus		331	TCTCAGCAGCGGAGCACTTCTCCATGATCTCTGCTCCCGCCACACAGTCAGGGCGCGCCCTTTGGGTGTGCTCTCTGCTCTGTCGGCCGAGGTGACCATTCCTGTTGCGGGTGTG	440
original1	BCY1	(329)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
MC50A19	BCY I	(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
MC50A6	BCY I	(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
MC50A8	BCY I	(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
MC54.21	BCY I	(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
MC55.29	BCY I	(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
MC55.32	BCY I	(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	
Consensus		(331)	CCCTACCGGCTGTGTGGGCTGTGGTGGTGGGCCCCAAGGGGCGAACCATCAAGGGCGATCCAGAGCAACCAACACATAATATATACACCAAGCCGTGACCGGACCCCGT	



FIGURE 3C

original BCY1	(878)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	990
MC50A19 BCY1	(881)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	
MC50A6 BCY1	(881)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	
MC50A8 BCY1	(881)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	
MC54.21 BCY1	(881)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	
MC55.29 BCY1	(881)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	
MC55.32 BCY1	(881)	CTATCCGCAAGGCGCGGCTTGGGCTCCCGGCGACACCGCTGCTCCCTGCTCCACTTTCGCGGACCCCGAGTGTGCCGGAATCTCCGAGGCTCCCGGAGAGAGCGGCTCCG	
Consensus		991	1100
original BCY1	(908)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
MC50A19 BCY1	(901)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
MC50A6 BCY1	(901)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
MC50A8 BCY1	(901)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
MC54.21 BCY1	(901)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
MC55.29 BCY1	(901)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
MC55.32 BCY1	(901)	GGCTTCTCTAAACTTGGTGGGCTGGGCTGCGGACGCTCCGAGGCTCCCGGCGGGAATTGCAAGGCTCTGTTTGAGAGCGAGTGAATGCGGCGCTTGTGTGCTGCGGACAA	
Consensus		1101	1210
original BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA----	
MC50A19 BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAAAGGAT	
MC50A6 BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAAAGGAT	
MC50A8 BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAAAGGAT	
MC54.21 BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA-----	
MC55.29 BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA-----	
MC55.32 BCY1	(1098)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA-----	
Consensus		1211	1249
original BCY1	(1204)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
MC50A19 BCY1	(1208)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
MC50A6 BCY1	(1208)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
MC50A8 BCY1	(1208)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
MC54.21 BCY1	(1204)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
MC55.29 BCY1	(1204)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
MC55.32 BCY1	(1204)	CAACCTGTCTTGCATGTGAGTGTGTAGTACACATCTTCGAGAGGAGCGGACCCAGAGTGTCCCGTCTGCGACATCATAGCCAGTAAAGCCATCCGGAATATTTCCTTAA	
Consensus		1211	1249

6/6

FIGURE 3D

MAELRLKGSS NTTECVPVPT SEHVAEIVGR QGCKIKALRA KNTYIKTPV RGEPPVEMVT GRREDVATAR REIISAEEHF SMIRASRNKS  
 GAAEGVAPAL PQQVTIRVRV PYRVVGLVVG PKGATIKRIQ QQTNTYIITP SRDRDPVFEI TCAPGNVERA REEIEITHIAV RTGKILEYNN  
 ENDFLAGSPD AAIDSRYSDA WRVHQFGCKP LSTFRQNSLG CIGECGVDSG FEAPRLCEQG GDFCYGGYLF PCYGVGKQDV YYGVAETSPP  
 LWAGQENATP TSVLFSSASS SSSSSAKARA GPPCAHRSPA TSAGPELAGL PRRPPCEPLQ GFSKLGGGGL RSPGGRDCM VCFESEVTAA  
 LVPCGHNLC MECAVRICER TDPECVCHI TAAQAIRIES